#4

SEQUENCE LISTING

<110> Bender, Eckhard

    Pindon, Armelle N

    Van Oers, Irma P

    Jurzak, Mirek

    Luyten, Walter H

<120> Cloning and expression of a novel 5-HT4 receptor

<130> Novel 5HT4B splice variant

<140> PCT/EP00/05592
<141> 2000-06-14

<150> GB/9913850.5
<151> 1999-06-14

<160> 2

<170> PatentIn Ver. 2.1

<210> 1
<211> 1281
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (4)..(1209)

<400> 1

```
gta atg gac aaa ctt gat gct aat gtg agt tct gag gag ggt ttc ggg   48
    Met Asp Lys Leu Asp Ala Asn Val Ser Ser Glu Glu Gly Phe Gly
    1               5                  10                  15

tca gtg gag aag gtg gtg ctg ctc acg ttt ctc tcg acg gtt atc ctg   96
```

Ser Val Glu Lys Val Val Leu Leu Thr Phe Leu Ser Thr Val Ile Leu
          20   25   30

atg gcc atc ttg ggg aac ctg ctg gtg atg gtg gct gtg tgc tgg gac   144
Met Ala Ile Leu Gly Asn Leu Leu Val Met Val Ala Val Cys Trp Asp
         35   40   45

agg cag ctc agg aaa ata aaa aca aat tat ttc att gta tct ctt gct   192
Arg Gln Leu Arg Lys Ile Lys Thr Asn Tyr Phe Ile Val Ser Leu Ala
        50   55   60

ttt gcg gat ctg ctg gtt tcg gtg ctg gtg atg ccc ttt ggt gcc att   240
Phe Ala Asp Leu Leu Val Ser Val Leu Val Met Pro Phe Gly Ala Ile
       65   70   75

gag ctg gtt caa gac atc tgg att tat ggg gag gtg ttt tgt ctt gtt   288
Glu Leu Val Gln Asp Ile Trp Ile Tyr Gly Glu Val Phe Cys Leu Val
80   85   90   95

cgg aca tct ctg gac gtc ctg ctc aca acg gca tcg att ttt cac ctg   336
Arg Thr Ser Leu Asp Val Leu Leu Thr Thr Ala Ser Ile Phe His Leu
        100   105   110

tgc tgc att tct ctg gat agg tat tac gcc atc tgc tgc cag cct ttg   384
Cys Cys Ile Ser Leu Asp Arg Tyr Tyr Ala Ile Cys Cys Gln Pro Leu
        115   120   125

gtc tat agg aac aag atg acc cct ctg cgc atc gca tta atg ctg gga   432
Val Tyr Arg Asn Lys Met Thr Pro Leu Arg Ile Ala Leu Met Leu Gly
        130   135   140

ggc tgc tgg gtc atc ccc acg ttt att tct ttt ctc cct ata atg caa   480
Gly Cys Trp Val Ile Pro Thr Phe Ile Ser Phe Leu Pro Ile Met Gln
        145   150   155

ggc tgg aat aac att ggc ata att gat ttg gaa agg agt cta aac caa   528
Gly Trp Asn Asn Ile Gly Ile Ile Asp Leu Glu Arg Ser Leu Asn Gln

```
                160           165           170           175

ggc ctg ggc cag gat ttt cat gcg ata gaa aag agg aag ttc aac cag   576
Gly Leu Gly Gln Asp Phe His Ala Ile Glu Lys Arg Lys Phe Asn Gln
          180           185           190


aac tct aac tct acg tac tgt gtc ttc atg gtc aac aag ccc tac gcc   624
Asn Ser Asn Ser Thr Tyr Cys Val Phe Met Val Asn Lys Pro Tyr Ala
          195           200           205


atc acc tgc tct gtg gtg gcc ttc tac atc cca ttt ctc ctc atg gtg   672
Ile Thr Cys Ser Val Val Ala Phe Tyr Ile Pro Phe Leu Leu Met Val
         210           215           220


ctg gcc tat tac cgc atc tat gtc aca gct aag gag cat gcc cat cag   720
Leu Ala Tyr Tyr Arg Ile Tyr Val Thr Ala Lys Glu His Ala His Gln
        225           230           235


atc cag atg tta caa cgg gca gga gcc tcc tcc gag agc agg cct cag   768
Ile Gln Met Leu Gln Arg Ala Gly Ala Ser Ser Glu Ser Arg Pro Gln
240           245           250           255


tcg gca gac cag cat agc act cat cgc atg agg aca gag acc aaa gca   816
Ser Ala Asp Gln His Ser Thr His Arg Met Arg Thr Glu Thr Lys Ala
          260           265           270


gcc aag acc ctg tgc atc atc atg ggt tgc ttc tgc ctc tgc tgg gca   864
Ala Lys Thr Leu Cys Ile Ile Met Gly Cys Phe Cys Leu Cys Trp Ala
          275           280           285


cca ttc ttt gtc acc aat att gtg gat cct ttc ata gac tac act gtc   912
Pro Phe Phe Val Thr Asn Ile Val Asp Pro Phe Ile Asp Tyr Thr Val
          290           295           300


cct ggg cag gtg tgg act gct ttc ctc tgg ctc ggc tat atc aat tcc   960
Pro Gly Gln Val Trp Thr Ala Phe Leu Trp Leu Gly Tyr Ile Asn Ser
         305           310           315
```

3

ggg ttg aac cct ttt ctc tac gcc ttc ttg aat aag tct ttt aga cgt   1008
Gly Leu Asn Pro Phe Leu Tyr Ala Phe Leu Asn Lys Ser Phe Arg Arg
320   325   330   335

gcc ttc ctc atc atc ctc tgc tgt gat gat gag cgc tac cga aga cct   1056
Ala Phe Leu Ile Ile Leu Cys Cys Asp Asp Glu Arg Tyr Arg Arg Pro
         340   345   350

tcc att ctg ggc cag act gtc cct tgt tca acc aca acc att aat gga   1104
Ser Ile Leu Gly Gln Thr Val Pro Cys Ser Thr Thr Thr Ile Asn Gly
          355   360   365

tcc aca cat gta cta agg gat gca gtg gag tgt ggt ggc cag tgg gag   1152
Ser Thr His Val Leu Arg Asp Ala Val Glu Cys Gly Gly Gln Trp Glu
          370   375   380

agt cag tgt cac ccg cca gca act tct cct ttg gtg gct gct cag ccc   1200
Ser Gln Cys His Pro Pro Ala Thr Ser Pro Leu Val Ala Ala Gln Pro
385   390   395

agt gac act taggcccctg ggacaatgac ccagaagaca gccatgcctc   1249
Ser Asp Thr
400

cgaaagaggg ccaggtccta agctgctgct tg   1281

<210> 2
<211> 402
<212> PRT
<213> Homo sapiens

<400> 2
Met Asp Lys Leu Asp Ala Asn Val Ser Ser Glu Glu Gly Phe Gly Ser
1   5   10   15

Val Glu Lys Val Val Leu Leu Thr Phe Leu Ser Thr Val Ile Leu Met
        20   25   30

Ala Ile Leu Gly Asn Leu Leu Val Met Val Ala Val Cys Trp Asp Arg
        35   40   45

Gln Leu Arg Lys Ile Lys Thr Asn Tyr Phe Ile Val Ser Leu Ala Phe
        50   55   60

Ala Asp Leu Leu Val Ser Val Leu Val Met Pro Phe Gly Ala Ile Glu
    65   70   75   80

Leu Val Gln Asp Ile Trp Ile Tyr Gly Glu Val Phe Cys Leu Val Arg
        85   90   95

Thr Ser Leu Asp Val Leu Leu Thr Thr Ala Ser Ile Phe His Leu Cys
       100   105   110

Cys Ile Ser Leu Asp Arg Tyr Tyr Ala Ile Cys Cys Gln Pro Leu Val
       115   120   125

Tyr Arg Asn Lys Met Thr Pro Leu Arg Ile Ala Leu Met Leu Gly Gly
       130   135   140

Cys Trp Val Ile Pro Thr Phe Ile Ser Phe Leu Pro Ile Met Gln Gly
145   150   155   160

Trp Asn Asn Ile Gly Ile Ile Asp Leu Glu Arg Ser Leu Asn Gln Gly
       165   170   175

Leu Gly Gln Asp Phe His Ala Ile Glu Lys Arg Lys Phe Asn Gln Asn
       180   185   190

Ser Asn Ser Thr Tyr Cys Val Phe Met Val Asn Lys Pro Tyr Ala Ile
       195   200   205

Thr Cys Ser Val Val Ala Phe Tyr Ile Pro Phe Leu Leu Met Val Leu

5

Ala Tyr Tyr Arg Ile Tyr Val Thr Ala Lys Glu His Ala His Gln Ile
225   230   235   240

Gln Met Leu Gln Arg Ala Gly Ala Ser Ser Glu Ser Arg Pro Gln Ser
          245   250   255

Ala Asp Gln His Ser Thr His Arg Met Arg Thr Glu Thr Lys Ala Ala
          260   265   270

Lys Thr Leu Cys Ile Ile Met Gly Cys Phe Cys Leu Cys Trp Ala Pro
          275   280   285

Phe Phe Val Thr Asn Ile Val Asp Pro Phe Ile Asp Tyr Thr Val Pro
          290   295   300

Gly Gln Val Trp Thr Ala Phe Leu Trp Leu Gly Tyr Ile Asn Ser Gly
305   310   315   320

Leu Asn Pro Phe Leu Tyr Ala Phe Leu Asn Lys Ser Phe Arg Arg Ala
          325   330   335

Phe Leu Ile Ile Leu Cys Cys Asp Asp Glu Arg Tyr Arg Arg Pro Ser
          340   345   350

Ile Leu Gly Gln Thr Val Pro Cys Ser Thr Thr Thr Ile Asn Gly Ser
          355   360   365

Thr His Val Leu Arg Asp Ala Val Glu Cys Gly Gly Gln Trp Glu Ser
          370   375   380

Gln Cys His Pro Pro Ala Thr Ser Pro Leu Val Ala Ala Gln Pro Ser
385   390   395   400

Asp Thr

6

<210> 3

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: PCR primer

<400> 3

cttcatggtc aacaagccct ac   22

<210> 4

<211> 28

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: PCR primer

<220>

<221> misc_feature

<222> (23)..(24)

<223> V = a or g or c; Y = t or c

<400> 4

cccgttgtaa catctggatt tgvygggc   28

<210> 5

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: DNA primer

<400> 5

gaaaggagtc taaaccaagg cct   23

<210> 6
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: DNA primer

<400> 6

cgcatgaaaa tcctggccca ggccttggtt   30

<210> 7
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: DNA primer

<400> 7

caagcagcag cttaggacct g   21

<210> 8
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: DNA primer

<400> 8

ccactcatgc ttatttcctg taatg   25

<210> 9

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: DNA primer

<220>

<221> misc_feature

<222> (2)

<223> R = g or a

<220>

<221> misc_feature

<222> (5)

<223> Y = t or c

<220>

<221> misc_feature

<222> (20)

<223> R = g or a

<220>

<221> misc_feature

<222> (23)

<223> y = t or c

<400> 9

graayaagat gacccctctr cgyatc   26

<210> 10

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:DNA primer

<220>

<221> misc_feature

<222> (5)..(6)

<223> r = g or a; n =a or g or t or c

<220>

<221> misc_feature

<222> (9)

<223> r = g or a

<400> 10

gcccrncara tccagatgtt acaacg   26

<210> 11

<211> 31

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: DNA primer

<220>

<221> misc_feature

<222> (10)..(11)

<223> R = g or a; y = a or g or t or c

<220>

<221> misc_feature

<222> (17)

10

<223> s = g or c

<220>

<221> misc_feature

<222> (26)

<223> r = g or a

<220>

<221> misc_feature

<222> (29)

<223> W = a or t

<400> 11

gtatgggcar yttctcsagt tcctgrtgwt g   31

<210> 12

<211> 29

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: DNA primer

<220>

<221> misc_difference

<222> (3)

<223> s = g or c

<220>

<221> misc_feature

<222> (10)..(12)

<223> n = a or g or t or c; v = a or g or c; r = g or a

<220>

<221> misc_feature

<222> (17)

<223> r = g or a

<220>
<221> misc_feature
<222> (21)
<223> y = t or c

<400> 12
gaasttgctg nvrggtgrca cygactctc   29

<210> 13
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: DNA primer

<400> 13
aaccaaggcc tgggccagga ttttcatggg   30